Figure 1

Match 70.5%; QryMatch 68.4%; Matches 572; Conservative 105; Mismatches 121;
Indels 13; Gaps 6;

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          ********  * *** **.  ****.***************** ******..*********
2PEP_m      1 MDQREILQQLLKEAQKGKLNSEEFASEFLKLKRQSTKYKADKIYPTTVAQRFKNIKGNRY  60
SuPTP04_h   1 MDQREILQKFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAEKPKNIKGGRY  60

          *******.* *****.***********.*************************.*******
2PEP_m     61 KDILPYDHSLVELSLLTSDEDSSYINASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEY 120
SuPTP04_h  61 KDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEY 120

          .*.*******.***********.**** ** *****.******.**** ***** ***.
2PEP_m    121 RILVIVMACMEFEMGKKKCERYWAEPGETQLQFGPFSISCEAEKKKSDYKIRTLKAKFNN 180
SuPTP04_h 121 SVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCZAEKRKSDYIIRTLKVKFNS 180

          ***.*******************.****.******* ******.***********.
2PEP_m    181 ETRIIYQFHYKNWPDHDVPSSIDPILQLIWDMRCYQEDDCVPICIHCSAGCGRTGVICAV 240
SuPTP04_h 181 ETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAI 240

          *************.*****.**.********************.********.****.
2PEP_m    241 DYTWMLLKDGIIPKNFSVFNLIQEMRTQRPSLVQTQEQYELVYSAVLELFKRHMDVIRDN 300
SuPTP04_h 241 DYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDK 300

          * * * ** ***  . *..***  .***...  * **.  .  * .** *
2PEP_m    301 HLGREIQAQCSIPEQSLTVEADSCPLDLPKNAMRDVKTTNQHSKQGAEAESTGGSSLGLR 360
SuPTP04_h 301 HSGTESQAKHCIPEQNHTLQADSYSPNLPKSTTKAAKMMNQQR---TKMEIKESSSFEFR 357

          ** ..* ****** **** **. **** . ...* * .*..* * .******* ****
2PEP_m    361 TSTMNAEEELVLHSAKSSPSFNCLELNCGCNNKAVITRNGQARASPVVGEPLQKYQSLDF 420
SuPTP04_h 358 TSEISAKEELVLHPAKSSTSFDFLELNYSFDKNADTTMKWQTKAFPIVGEPLQKHQSLDL 417

          **.** .*... *.*.* ** *** *. ************** *... ** **** *
2PEP_m    421 GSMLFGSCPSALPINTADRYHNSKGPVKRTKSTPFELIQQRKTNDLAVGDGFSCLESQLH 480
SuPTP04_h 418 GSLLFEGCSNSKPVNAAGRYFNSKVPITRTKSTPFELIQQRETKEVDSKENFSYLESQPH 477

          .  . *.* *.* **** *******        .** *.* ..** * * .* *.**
2PEP_m    481 EHYSLRELQVQRVAHVSSEELNYSLPGAC-----DASCVPRHSPGALRVHLYTSLAEDPY 535
SuPTP04_h 478 DSCFV-EMQAQKVMHVSSAELNYSLPYDSKHQIRNASNVKHHDSSALGVYSYIPLVENPY 536

          *** **... **** *********.  *..***.***. * *.**** .*. *. *. *
2PEP_m    536 FSSSPPNSADSKMSFDLPEKQDGATSPGALLPASSTTSPFYSNPHDSLVMNTLTSFSPPL 595
SuPTP04_h 537 FSSWPPSGTSSKMSLDLPEKQDGTVFPSSLLPTSSTSLPSYYNSHDSLSLNSPTNISSLL 596

          ***.** * . * ********* ************.***** ** * **.  * *.* *
2PEP_m    596 NQETAVEAPSRRTDDEIPPPLPERTPESFIVVEEAGEPSPRVTESLP--LVVTFGASPEC 653
SuPTP04_h 597 NQESAVLATAPRIDDEIPPPLPVRTPESFIVVEEAGEFSPNVPKSLSSAVKVKIGTSLEW 656

          .****  .*  ***   ***.*******. *** .*********************.***
2PEP_m    654 SGTSE-MKSHDSVGFTPSKNVKLRSPKSDRHQD-GSPPPPLPERTLESFFLADEDCICAQ 711
SuPTP04_h 657 GGTSEPKKFDDSVILRPSKSVKLRSPKSELHQDRSSPPPPLPERTLESFFLADEDCMCAQ 716

          ...* ******.* **********.**************** ****** *** .*.**.* **
2PEP_m    712 AVQTSSTSYPETTENSTSSKQTLRTPGKSFTRSKSLKIFRNMKKSVCNSSSPSKPTERVQ 771
SuPTP04_h 717 SIETYSTSYPDTMENSTSSKQTLKTPGKSFTRSKSLKILRNMKKSICNSCFFNKPAESVQ 776

          ..*********.************** .**.
2PEP_m    772 PKNSSSFLNFGFGNRFSKPKGPRNPPSAWNM 802
SuPTP04_h 777 SNNSSSFLNFGFANRFSKPKGPRNPPPTWNI 807
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